



Sequence Listing

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TECH CENTER 1600/2900

<110> Lasky, Laurence A.
Dowbenko, Donald J.

<120> Tyrosine Phosphorylated Cleavage Furrow-Associated
Proteins (PSTPIPs)

<130> P1066P2

<140> US 09/068,377

<141> 1998-05-08

<150> PCT/US98/01774

<151> 1998-01-30

<150> US 08/938,830

<151> 1997-09-29

<150> US 60/104,589

<151> 1997-02-07

<160> 73

<210> 1

<211> 415

<212> PRT

<213> Mus Musculus

<400> 1

Met	Met	Ala	Gln	Leu	Gln	Phe	Arg	Asp	Ala	Phe	Trp	Cys	Arg	Asp
1				5					10					15

Phe	Thr	Ala	His	Thr	Gly	Tyr	Glu	Val	Leu	Leu	Gln	Arg	Leu	Leu
				20					25					30

Asp	Gly	Arg	Lys	Met	Cys	Lys	Asp	Val	Glu	Glu	Leu	Leu	Arg	Gln
			35						40					45

Arg	Ala	Gln	Ala	Glu	Glu	Arg	Tyr	Gly	Lys	Glu	Leu	Val	Gln	Ile
				50					55					60

Ala	Arg	Lys	Ala	Gly	Gly	Gln	Thr	Glu	Met	Asn	Ser	Leu	Arg	Thr
				65					70					75

Ser	Phe	Asp	Ser	Leu	Lys	Gln	Gln	Thr	Glu	Asn	Val	Gly	Ser	Ala
				80					85					90

His	Ile	Gln	Leu	Ala	Leu	Ala	Leu	Arg	Glu	Glu	Leu	Arg	Ser	Leu
				95					100					105

Glu	Glu	Phe	Arg	Glu	Arg	Gln	Lys	Glu	Gln	Arg	Lys	Lys	Tyr	Glu
				110					115					120

Ala	Ile	Met	Asp	Arg	Val	Gln	Lys	Ser	Lys	Leu	Ser	Leu	Tyr	Lys
				125					130					135

Lys Thr Met Glu Ser Lys Lys Ala Tyr Asp Gln Lys Cys Arg Asp	140	145	150
Ala Asp Asp Ala Glu Gln Ala Phe Glu Arg Val Ser Ala Asn Gly	155	160	165
His Gln Lys Gln Val Glu Lys Ser Gln Asn Lys Ala Lys Gln Cys	170	175	180
Lys Glu Ser Ala Thr Glu Ala Glu Arg Val Tyr Arg Gln Asn Ile	185	190	195
Glu Gln Leu Glu Arg Ala Arg Thr Glu Trp Glu Gln Glu His Arg	200	205	210
Thr Thr Cys Glu Ala Phe Gln Leu Gln Glu Phe Asp Arg Leu Thr	215	220	225
Ile Leu Arg Asn Ala Leu Trp Val His Cys Asn Gln Leu Ser Met	230	235	240
Gln Cys Val Lys Asp Asp Glu Leu Tyr Glu Glu Val Arg Leu Thr	245	250	255
Leu Glu Gly Cys Asp Val Glu Gly Asp Ile Asn Gly Phe Ile Gln	260	265	270
Ser Lys Ser Thr Gly Arg Glu Pro Pro Ala Pro Val Pro Tyr Gln	275	280	285
Asn Tyr Tyr Asp Arg Glu Val Thr Pro Leu Ile Gly Ser Pro Ser	290	295	300
Ile Gln Pro Ser Cys Gly Val Ile Lys Arg Phe Ser Gly Leu Leu	305	310	315
His Gly Ser Pro Lys Thr Thr Pro Ser Ala Pro Ala Ala Ser Thr	320	325	330
Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu Leu Val Tyr Ala	335	340	345
Ser Ile Glu Val Gln Ala Thr Gln Gly Asn Leu Asn Ser Ser Ala	350	355	360
Gln Asp Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp	365	370	375
Glu Leu Asp Ile Ser Ala Gly Asp Ile Leu Ala Val Ile Leu Glu	380	385	390
Gly Glu Asp Gly Trp Trp Thr Val Glu Arg Asn Gly Gln Arg Gly	395	400	405
Phe Val Pro Gly Ser Tyr Leu Glu Lys Leu	410	415	

<210> 2
<211> 2100
<212> DNA
<213> Mus Musculus

<400> 2
caatattttca agctataacca agcatacaat caactccaag cttatgccca 50
agaagaagcg gaaggtctcg agcggcgcca attttaatca aagtgggaat 100
attgctgata gctcattgtc cttcactttc actaacagta gcaacgggtcc 150
gaacctcata acaactcaaa caaattctca agcgctttca caaccaattg 200
cctcctctaa cgttcatgat aacttcatga ataatgaaat cacggctagt 250
aaaattgatg atggtaataa ttcaaaacca ctgtcacctg gttggacgga 300
ccaaactgcg tataacgcgt ttggaatcac tacagggatg tttaatacca 350
ctacaatgga tgatgtatat aactatctat tcgatgatga agatacccca 400
ccaaacccaa aaaaagaggg tgggtcgacc cacgcgtccg gtccttctct 450
catttcgctg ctgattctag ccccaaacia aacaggttga gcctttttcc 500
tcctccggca gttgcctctg gcttgtggct gccttctgag cgtttcagac 550
ggcgccggct gggagtggga gggagggcct gggctagccg cgctgggact 600
gggacgtgct cctggctcct ggcccatgct cagccctgct tgaagcagga 650
gtgctagcat ttgacacaac gcccttggag gatgatggcc cagctgcagt 700
tccgagatgc cttctgggtgc agggacttca cggcccacac agggtatgag 750
gtgctactgc agaggctgct ggacggcagg aagatgtgca aggatgtgga 800
ggagctgctc agacagaggg cccagggcga ggagaggtac gggaaggagc 850
tggtgcagat tgcacgcaag gctggtggcc agacagagat gaattccctg 900
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acacatccag ctggccctgg ccctgcgtga ggagctgcgg agcctggagg 1000
agttccgaga gagacagaaa gagcagcgga agaagtatga ggccatcatg 1050
gaccgtgtcc agaagagcaa gttgtcgctc tacaagaaga ccatggagtc 1100
caagaaggca tatgaccaga agtgcaggga tgcagatgat gctgagcagg 1150
ccttcgagcg tgtgagtgcc aatggccacc agaagcaagt agaaaagagc 1200
cagaacaaag ccaagcagtg caaggagtca gccacagagg cagaaagagt 1250
gtacaggcaa aatatcgaac aactggagag agcgaggacc gagtgggagc 1300

agggagcaccg gactacctgt gaggccttcc agttgcagga gtttgaccgg 1350
 ctcaccatcc tccgcaatgc cctgtgggtg cactgtaacc agctctccat 1400
 gcagtgtgtc aaggatgatg agctctatga ggaagtgcgg ctgacccttg 1450
 agggctgtga tgtggaaggt gacatcaatg gcttcatcca gtccaagagc 1500
 actggcagag agccccagc tccggtgcct taccagaact actatgacag 1550
 ggaggtgacc ccactgattg gcagccctag catccagccc tcttgcggtg 1600
 tgataaagag gttctctggg ctgctacatg gaagtcccaa gaccacacct 1650
 tctgctcctg ctgcttcac agagactctg actcccaccc ctgagcggaa 1700
 tgagttggtc tacgcatcca tcgaagtga ggcgaccag ggaaacctta 1750
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 tctgatgagc tggacatttc cgcgggagac atcctggcgg tcatcctgga 1850
 aggggaggat ggctgggtga ctgtggagcg gaacggacaa cgtggctttg 1900
 tccctgggtc gtacttgag aagctctgag gaaaggctag cagtctccac 1950
 atacctccgc cctgactgtg aggtcaggac tgtttctttc catcaccgcc 2000
 caggcctcac ggggccagaa ccaagcccgg tgggtgctggg catgggctgg 2050
 gtgctggcta ctctcaataa atgtctccca gaaggaaaaa aaaaaaaaaa 2100

<210> 3

<211> 48

<212> PRT

<213> Mus Musculus

<400> 3

Leu	Tyr	Asp	Tyr	Thr	Ala	Gln	Asn	Ser	Asp	Glu	Leu	Asp	Ile	Ser
1				5				10					15	

Ala	Gly	Asp	Ile	Leu	Ala	Val	Ile	Leu	Glu	Gly	Glu	Asp	Gly	Trp
				20				25					30	

Trp	Thr	Val	Glu	Arg	Asn	Gly	Gln	Arg	Gly	Phe	Val	Pro	Gly	Ser
				35				40					45	

Tyr Leu Arg

<210> 4

<211> 50

<212> PRT

<213> Homo sapien

<400> 4

Leu Tyr Gln Tyr Ile Gly Gln Asp Val Asp Glu Leu Ser Phe Asn
1 5 10 15

Val Asn Glu Val Ile Glu Ile Leu Ile Glu Asp Ser Ser Gly Trp
20 25 30

Trp Lys Gly Arg Leu His Gly Gln Glu Gly Leu Phe Pro Gly Asn
35 40 45

Tyr Val Glu Lys Ile
50

<210> 5

<211> 50

<212> PRT

<213> Homo sapien

<400> 5

Leu Tyr Asp Tyr Gln Glu Lys Ser Pro Arg Glu Val Thr Met Lys
1 5 10 15

Lys Gly Asp Ile Leu Thr Leu Leu Asn Ser Thr Asn Lys Asp Trp
20 25 30

Trp Lys Val Glu Val Asn Asp Arg Gln Gly Phe Val Pro Ala Ala
35 40 45

Tyr Val Lys Lys Leu
50

<210> 6

<211> 50

<212> PRT

<213> Homo sapien

<400> 6

Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser Phe Asp
1 5 10 15

Pro Asp Asp Ile Ile Thr Asp Ile Glu Met Val Asp Glu Gly Trp
20 25 30

Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu Phe Pro Ala Asn
35 40 45

Tyr Val Lys Leu Leu
50

<210> 7

<211> 48

<212> PRT

<213> Homo sapien

<400> 7

Leu Tyr Asp Tyr Gln Ala Ala Gly Asp Asp Glu Ile Ser Phe Asp
1 5 10 15

Pro Asp Asp Ile Ile Thr Asn Ile Glu Met Ile Asp Asp Gly Trp
20 25 30

Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu Phe Pro Ala Asn
35 40 45

Tyr Val Glu

<210> 8

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid epitope tag

<400> 8

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 9

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 9

cgcgatcca ccatgatggc ccagctgcag ttc 33

<210> 10

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 10

gtacgcgtcg actcacttgt catcgtcgtc cttgtagtcg agctt 45

<210> 11

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 11

tgcctttctc tccacagg 18

<210> 12

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 12

ctccttgagg ttctactagt gggggctggt gtcctg 36

<210> 13

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13

gcggcgcac tagtatccag tctgtgctcc atctgttac 39

<210> 14

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14

gcgtttggaa tcactac 17

<210> 15

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15

ttatagttta gcggcgcgtc accggtagtc ctgggctgat g 41

<210> 16

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 16

gtacgcgtcg accgcactct acgactacac tgcacag 37

<210> 17

<211> 17

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
ctctggcgaa gaagtcc 17

<210> 18
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
gatcgaattc ccagaacctc aaggagaact gc 32

<210> 19
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
gatcctcgag ttacaccggt gtccactctg ctggagga 38

<210> 20
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 20
Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro
1 5 10 15

Pro Ala Glu Trp Thr
20

<210> 21
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 21
Gly Phe Gly Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro
1 5 10 15

Pro Ser Ala Trp

<210> 22
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 22
Gly Phe Gly Asn Arg Cys Gly Lys Pro Lys Gly Pro Arg Asp Pro
1 5 10 15
Pro Ser Glu Trp Thr
20

<210> 23
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 23
Gly Gly Val Leu Arg Ser Ile Ser Val Pro Ala Pro Pro Thr Leu
1 5 10 15
Pro Met Ala Asp Thr
20

<210> 24
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
gtatatgtcc tggccagccc atgggggttcc cagcag 36

<210> 25
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
gcaggtcgac tctagattac acccgtgtcc actctg 36

<210> 26
<211> 907
<212> PRT
<213> Saccharomyces Pombe

<400> 26

Met	Leu	Thr	Lys	Ser	Leu	Gln	Gly	Ser	Glu	Asp	Ala	Gly	Met	Asp
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Ala	Leu	Met	Ser	Arg	Thr	Lys	Ser	Ser	Leu	Ser	Val	Leu	Glu	Ser
				20					25					30
Ile	Asp	Glu	Phe	Tyr	Ala	Lys	Arg	Ala	Ser	Ile	Glu	Arg	Glu	Tyr
				35					40					45
Ala	Ser	Lys	Leu	Gln	Glu	Leu	Ala	Ala	Ser	Ser	Ala	Asp	Ile	Pro
				50					55					60
Glu	Val	Gly	Ser	Thr	Leu	Asn	Asn	Ile	Leu	Ser	Met	Arg	Thr	Glu
				65					70					75
Thr	Gly	Ser	Met	Ala	Lys	Ala	His	Glu	Glu	Val	Ser	Gln	Gln	Ile
				80					85					90
Asn	Thr	Glu	Leu	Arg	Asn	Lys	Ile	Arg	Glu	Tyr	Ile	Asp	Gln	Thr
				95					100					105
Glu	Gln	Gln	Lys	Val	Val	Ala	Ala	Asn	Ala	Ile	Glu	Glu	Leu	Tyr
				110					115					120
Gln	Lys	Lys	Thr	Ala	Leu	Glu	Ile	Asp	Leu	Ser	Glu	Lys	Lys	Asp
				125					130					135
Ala	Tyr	Glu	Tyr	Ser	Cys	Asn	Lys	Leu	Asn	Ser	Tyr	Met	Arg	Gln
				140					145					150
Thr	Lys	Lys	Met	Thr	Gly	Arg	Glu	Leu	Asp	Lys	Tyr	Asn	Leu	Lys
				155					160					165
Ile	Arg	Gln	Ala	Ala	Leu	Ala	Val	Lys	Lys	Met	Asp	Ala	Glu	Tyr
				170					175					180
Arg	Glu	Thr	Asn	Glu	Leu	Leu	Leu	Thr	Val	Thr	Arg	Glu	Trp	Ile
				185					190					195
Asp	Arg	Trp	Thr	Glu	Val	Cys	Asp	Ala	Phe	Gln	His	Ile	Glu	Glu
				200					205					210
Tyr	Arg	Leu	Glu	Phe	Leu	Lys	Thr	Asn	Met	Trp	Ala	Tyr	Ala	Asn
				215					220					225
Ile	Ile	Ser	Thr	Ala	Cys	Val	Lys	Asp	Asp	Glu	Ser	Cys	Glu	Lys
				230					235					240
Ile	Arg	Leu	Thr	Leu	Glu	Asn	Thr	Asn	Ile	Asp	Glu	Asp	Ile	Thr
				245					250					255
Gln	Met	Ile	Gln	Asn	Glu	Gly	Thr	Gly	Thr	Thr	Ile	Pro	Pro	Leu
				260					265					270
Pro	Glu	Phe	Asn	Asp	Tyr	Phe	Lys	Glu	Asn	Gly	Leu	Asn	Tyr	Asp

	275	280	285
Ile Asp Gln Leu	Ile Ser Lys Ala Pro	Ser Tyr Pro Tyr Ser	Ser Ser
	290	295	300
Ser Arg Pro Ser	Ala Ser Ala Ser Leu	Ala Ser Ser Pro Thr	Arg
	305	310	315
Ser Ala Phe Arg	Pro Lys Thr Ser Glu	Thr Val Ser Ser Glu	Val
	320	325	330
Val Ser Ser Pro	Pro Thr Ser Pro Leu	His Ser Pro Val Lys	Pro
	335	340	345
Val Ser Asn Glu	Gln Val Glu Gln Val	Thr Glu Val Glu Leu	Ser
	350	355	360
Ile Pro Val Pro	Ser Ile Gln Glu Ala	Glu Ser Gln Lys Pro	Val
	365	370	375
Leu Thr Gly Ser	Ser Met Arg Arg Pro	Ser Val Thr Ser Pro	Thr
	380	385	390
Phe Glu Val Ala	Ala Arg Pro Leu Thr	Ser Met Asp Val Arg	Ser
	395	400	405
Ser His Asn Ala	Glu Thr Glu Val Gln	Ala Ile Pro Ala Ala	Thr
	410	415	420
Asp Ile Ser Pro	Glu Val Lys Glu Gly	Lys Asn Ser Glu Asn	Ala
	425	430	435
Ile Thr Lys Asp	Asn Asp Asp Ile Ile	Leu Ser Ser Gln Leu	Gln
	440	445	450
Pro Thr Ala Thr	Gly Ser Arg Ser Ser	Arg Leu Ser Phe Ser	Arg
	455	460	465
His Gly His Gly	Ser Gln Thr Ser Leu	Gly Ser Ile Lys Arg	Lys
	470	475	480
Ser Ile Met Glu	Arg Met Gly Arg Pro	Thr Ser Pro Phe Met	Gly
	485	490	495
Ser Ser Phe Ser	Asn Met Gly Ser Arg	Ser Thr Ser Pro Thr	Lys
	500	505	510
Glu Gly Phe Ala	Ser Asn Gln His Ala	Thr Gly Ala Ser Val	Gln
	515	520	525
Ser Asp Glu Leu	Glu Asp Ile Asp Pro	Arg Ala Asn Val Val	Leu
	530	535	540
Asn Val Gly Pro	Asn Met Leu Ser Val	Gly Glu Ala Pro Val	Glu
	545	550	555
Ser Thr Ser Lys	Glu Glu Asp Lys Asp	Val Pro Asp Pro Ile	Ala

560										565				570			
Asn	Ala	Met	Ala	Glu	Leu	Ser	Ser	Ser	Met	Arg	Arg	Arg	Gln	Ser			
				575					580					585			
Thr	Ser	Val	Asp	Asp	Glu	Ala	Pro	Val	Ser	Leu	Ser	Lys	Thr	Ser			
				590					595					600			
Ser	Ser	Thr	Arg	Leu	Asn	Gly	Leu	Gly	Tyr	His	Ser	Arg	Asn	Thr			
				605					610					615			
Ser	Ile	Ala	Ser	Asp	Ile	Asp	Gly	Val	Pro	Lys	Lys	Ser	Thr	Leu			
				620					625					630			
Gly	Ala	Pro	Pro	Ala	Ala	His	Thr	Ser	Ala	Gln	Met	Gln	Arg	Met			
				635					640					645			
Ser	Asn	Ser	Phe	Ala	Ser	Gln	Thr	Lys	Gln	Val	Phe	Gly	Glu	Gln			
				650					655					660			
Arg	Thr	Glu	Asn	Ser	Ala	Arg	Glu	Ser	Leu	Arg	His	Ser	Arg	Ser			
				665					670					675			
Asn	Met	Ser	Arg	Ser	Pro	Ser	Pro	Met	Leu	Ser	Arg	Arg	Ser	Ser			
				680					685					690			
Thr	Leu	Arg	Pro	Ser	Phe	Glu	Arg	Ser	Ala	Ser	Ser	Leu	Ser	Val			
				695					700					705			
Arg	Gln	Ser	Asp	Val	Val	Ser	Pro	Ala	Pro	Ser	Thr	Arg	Ala	Arg			
				710					715					720			
Gly	Gln	Ser	Val	Ser	Gly	Gln	Gln	Arg	Pro	Ser	Ser	Ser	Met	Ser			
				725					730					735			
Leu	Tyr	Gly	Glu	Tyr	Asn	Lys	Ser	Gln	Pro	Gln	Leu	Ser	Met	Gln			
				740					745					750			
Arg	Ser	Val	Ser	Pro	Asn	Pro	Leu	Gly	Pro	Asn	Arg	Arg	Ser	Ser			
				755					760					765			
Ser	Val	Leu	Gln	Ser	Gln	Lys	Ser	Thr	Ser	Ser	Asn	Thr	Ser	Asn			
				770					775					780			
Arg	Asn	Asn	Gly	Gly	Tyr	Ser	Gly	Ser	Arg	Pro	Ser	Ser	Glu	Met			
				785					790					795			
Gly	His	Arg	Tyr	Gly	Ser	Met	Ser	Gly	Arg	Ser	Met	Arg	Gln	Val			
				800					805					810			
Ser	Gln	Arg	Ser	Thr	Ser	Arg	Ala	Arg	Ser	Pro	Glu	Pro	Thr	Asn			
				815					820					825			
Arg	Asn	Ser	Val	Gln	Ser	Lys	Asn	Val	Asp	Pro	Arg	Ala	Thr	Phe			
				830					835					840			
Thr	Ala	Glu	Gly	Glu	Pro	Ile	Leu	Gly	Tyr	Val	Ile	Ala	Leu	Tyr			

	845		850		855
Asp Tyr Gln Ala Gln Ile Pro Glu Glu Ile Ser Phe Gln Lys Gly					
	860		865		870
Asp Thr Leu Met Val Leu Arg Thr Gln Glu Asp Gly Trp Trp Asp					
	875		880		885
Gly Glu Ile Ile Asn Val Pro Asn Ser Lys Arg Gly Leu Phe Pro					
	890		895		900
Ser Asn Phe Val Gln Thr Val					
	905				

<210> 27

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> This is a consensus sequence representing yeast and mice.

<221> Variant

<222> (2)...(3)

<223> Xaa = any amino acid

<400> 27

Pro Xaa Xaa Pro

1

<210> 28

<211> 1613

<212> DNA

<213> Homo sapien

<400> 28

acgatcacta tagggcgaat tgggcctcta gatgcatgct cgagcggccg 50

ccagtgtgat ggatatctgc agaattcggc ttccatccta atacgactca 100

ctatagggct cgagcggccg cccgggcagg tctagaattc agcggccgct 150

gaattctctt tttcctcccc tcagaagctc ctctctggct cgtggctgcc 200

ttctgagtgt tgcagacggc gccggccggg aaggggggcc tgggccagcc 250

ctgccaggac tgggacgctg ctgctgacgc ctggccctcc atcaggccag 300

cctgtggcag gagagtgagc tttgccgcgg cagacgcctg aggatgatgc 350

cccagctgca gttcaaagat gccttttggg gcagggactt cacagcccac 400

acgggctacg aggtgctgct gcagcggcct ctggatggca ggaagatgtg 450

caaagacatg gaggagctac tgaggcagag ggcccaggcg gaggagcggc 500

acgggaagga gctggtgcag atcgcacgga aggcaggtgg ccagacggag 550

atcaactccc tgagggcctc ctttgactcc ttgaagcagc aaatggagaa 600
 tgtgggcagc tcacacatcc agctggccct gaccctgctg gaggagctgc 650
 ggagtctcga ggagtttcgt gagaggcaga aggagcagag gaagaagggc 700
 atggctgtcc cgagacagag tgactgcatg gaagtgaagt ccccatcatg 750
 ggagtatgag gccgtcatgg accgggtcca gaagagcaag ctgtcgtctt 800
 acaagaaggc catggagtcc aagaagacat acgagcagaa gtgccgggac 850
 gcggacgacg cggagcaggc cttcgagcgc attagcgcca acggccacca 900
 gaagcaggtg gagaagagtc agaacaaagc caggcagtgc aaggactcgg 950
 ccaccgaggc agagcgggta tacaggcaga gcattgcgca gctggagaag 1000
 gtccgggctg agtgggagca ggagcaccgg accacctgtg aggcctttca 1050
 gctgcaagag tttagaccggc tgaccattct ccgcaacgcc ctgtgggtgc 1100
 acagtaacca gctctccatg cagtgtgtca aggatgatga gctctacgag 1150
 gaagtgcggc tgacgctgga aggtgcagc atagacgccg acatcgacag 1200
 tttcatccag gccaaagagca cgggcacaga gccccccagg ttctctggac 1250
 tgctgcacgg aagtcccaag accacttcgt cagcttctgc tggctccaca 1300
 gagaccctga cccccacccc cgagcggaat gagggtgtct acacagccat 1350
 cgcagtgcag gagatacagg gaaaccggc ctaccagcc caggactacc 1400
 gggcgctcta cgattataca gcgcagaacc cagatgagct ggacctgtcc 1450
 gcgggagaca tcctggaagg ggaggatggc tggaggactg tggagaggaa 1500
 cgggcagcgt ggcttcgtcc ctggttccta cctggagaag ctttgaggga 1550
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 cccagcact gtc 1613

<210> 29

<211> 400

<212> PRT

<213> Homo sapien

<400> 29

Met	Met	Pro	Gln	Leu	Gln	Phe	Lys	Asp	Ala	Phe	Trp	Cys	Arg	Asp
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Phe	Thr	Ala	His	Thr	Gly	Tyr	Glu	Val	Leu	Leu	Gln	Arg	Leu	Leu
				20					25					30

Asp	Gly	Arg	Lys	Met	Cys	Lys	Asp	Met	Glu	Glu	Leu	Leu	Arg	Gln	
				35					40					45	
Arg	Ala	Gln	Ala	Glu	Glu	Arg	Tyr	Gly	Lys	Glu	Leu	Val	Gln	Ile	
				50					55					60	
Ala	Arg	Lys	Ala	Gly	Gly	Gln	Thr	Glu	Ile	Asn	Ser	Leu	Arg	Ala	
				65					70					75	
Ser	Phe	Asp	Ser	Leu	Lys	Gln	Gln	Met	Glu	Asn	Val	Gly	Ser	Ser	
				80					85					90	
His	Ile	Gln	Leu	Ala	Leu	Thr	Leu	Arg	Glu	Glu	Leu	Arg	Ser	Leu	
				95					100					105	
Glu	Glu	Phe	Arg	Glu	Arg	Gln	Lys	Glu	Gln	Arg	Lys	Lys	Gly	Met	
				110					115					120	
Ala	Val	Pro	Arg	Gln	Ser	Asp	Cys	Met	Glu	Val	Lys	Ser	Pro	Ser	
				125					130					135	
Trp	Glu	Tyr	Glu	Ala	Val	Met	Asp	Arg	Val	Gln	Lys	Ser	Lys	Leu	
				140					145					150	
Ser	Leu	Tyr	Lys	Lys	Ala	Met	Glu	Ser	Lys	Lys	Thr	Tyr	Glu	Gln	
				155					160					165	
Lys	Cys	Arg	Asp	Ala	Asp	Asp	Ala	Glu	Gln	Ala	Phe	Glu	Arg	Ile	
				170					175					180	
Ser	Ala	Asn	Gly	His	Gln	Lys	Gln	Val	Glu	Lys	Ser	Gln	Asn	Lys	
				185					190					195	
Ala	Arg	Gln	Cys	Lys	Asp	Ser	Ala	Thr	Glu	Ala	Glu	Arg	Val	Tyr	
				200					205					210	
Arg	Gln	Ser	Ile	Ala	Gln	Leu	Glu	Lys	Val	Arg	Ala	Glu	Trp	Glu	
				215					220					225	
Gln	Glu	His	Arg	Thr	Thr	Cys	Glu	Ala	Phe	Gln	Leu	Gln	Glu	Phe	
				230					235					240	
Asp	Arg	Leu	Thr	Ile	Leu	Arg	Asn	Ala	Leu	Trp	Val	His	Ser	Asn	
				245					250					255	
Gln	Leu	Ser	Met	Gln	Cys	Val	Lys	Asp	Asp	Glu	Leu	Tyr	Glu	Glu	
				260					265					270	
Val	Arg	Leu	Thr	Leu	Glu	Gly	Cys	Ser	Ile	Asp	Ala	Asp	Ile	Asp	
				275					280					285	
Ser	Phe	Ile	Gln	Ala	Lys	Ser	Thr	Gly	Thr	Glu	Pro	Pro	Arg	Phe	
				290					295					300	
Ser	Gly	Leu	Leu	His	Gly	Ser	Pro	Lys	Thr	Thr	Ser	Ser	Ala	Ser	
				305					310					315	

Ala Gly Ser Thr Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu		
	320	330
Gly Val Tyr Thr Ala Ile Ala Val Gln Glu Ile Gln Gly Asn Pro		
	335	345
Ala Ser Pro Ala Gln Asp Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala		
	350	360
Gln Asn Pro Asp Glu Leu Asp Leu Ser Ala Gly Asp Ile Leu Glu		
	365	375
Gly Glu Asp Gly Trp Trp Thr Val Glu Arg Asn Gly Gln Arg Gly		
	380	390
Phe Val Pro Gly Ser Tyr Leu Glu Lys Leu		
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<210> 33
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<212> DNA

<213> Artificial Sequence

<220>

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<210> 35

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<210> 37

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<400> 37

ttgacctcga gtcatcaccg ctcaggggtg ggagtcagag tc 42

<210> 38

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<400> 58

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gatgtcacct tccacatcgg agccctcaag ggtcag 36

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gttacacccg tgcgcctct gcaggaggat cccg 34